



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/743,752A

DATE: 04/03/2003

TIME: 14:25:11

Input Set : A:\pf0559usn_seqlist.txt

Output Set: N:\CRF4\04032003\I743752A.raw

5 <110> APPLICANT: INCYTE PHARMACEUTICALS, INC.
6 BANDMAN, Olga
7 TANG, Y. Tom
8 CORLEY, Neil C.
9 AZIMZAI, Yalda
10 BAUGHN, Mariah R.
12 <120> TITLE OF INVENTION: HUMAN SCAD-RELATED MOLECULES, SCRM-1 AND SCRM-2
14 <130> FILE REFERENCE: PF-0559 USN
16 <140> CURRENT APPLICATION NUMBER: 09/743,752A
C--> 17 <141> CURRENT FILING DATE: 2003-02-11
19 <150> PRIOR APPLICATION NUMBER: PCT/US9916164
20 <151> PRIOR FILING DATE: 1999-07-16
22 <150> PRIOR APPLICATION NUMBER: US 09/116,750
23 <151> PRIOR FILING DATE: 1998-07-16
25 <150> PRIOR APPLICATION NUMBER: US 60/160,074
26 <151> PRIOR FILING DATE: 1998-07-16
28 <160> NUMBER OF SEQ ID NOS: 6
30 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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34 <212> TYPE: PRT
35 <213> ORGANISM: HOMO SAPIENS
37 <220> FEATURE:
38 <221> NAME/KEY: misc_feature
39 <223> OTHER INFORMATION: Incyte Clone No: 1240869
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44 Val Arg Met Ala Ser Ser Arg Met Thr Arg Arg Asp Pro Leu Thr Asn
45 20 25 30
46 Lys Val Ala Leu Val Thr Ala Ser Thr Asp Gly Ile Gly Phe Ala Ile
47 35 40 45
48 Ala Arg Arg Leu Ala Gln Asp Arg Ala His Val Val Val Ser Ser Arg
49 50 55 60
50 Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr Leu Gln Gly Glu Gly
51 65 70 75 80
52 Leu Ser Val Thr Gly Thr Val Cys His Val Gly Lys Ala Glu Asp Arg
53 85 90 95
54 Glu Arg Leu Val Ala Thr Ala Val Lys Leu His Gly Gly Ile Asp Ile
55 100 105 110
56 Leu Val Ser Asn Ala Ala Val Asn Pro Phe Phe Gly Ser Ile Met Asp
57 115 120 125
58 Val Thr Glu Glu Val Trp Asp Lys Thr Leu Asp Ile Asn Val Lys Ala

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61 145      150      155      160
62 Gly Gly Ser Val Val Ile Val Ser Ser Ile Ala Ala Phe Ser Pro Ser
63      165      170      175
64 Pro Gly Phe Ser Pro Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu
65      180      185      190
66 Asn Asn Thr Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile Arg Val Asn
67      195      200      205
68 Cys Leu Ala Pro Gly Leu Ile Lys Thr Ser Phe Ser Arg Met Leu Trp
69      210      215      220
70 Met Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
71 225      230      235      240
72 Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu Cys
73      245      250      255
74 Ser Glu Asp Ala Ser Tyr Ile Thr Gly Glu Thr Val Val Val Gly Gly
75      260      265      270
76 Gly Thr Pro Ser Arg Leu
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80 <211> LENGTH: 564
81 <212> TYPE: PRT
82 <213> ORGANISM: HOMO SAPIENS
84 <220> FEATURE:
85 <221> NAME/KEY: misc_feature
86 <223> OTHER INFORMATION: Incyte Clone No: 2060002
88 <400> SEQUENCE: 2
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91 Tyr Ala Tyr Pro Ser Asp Tyr Asp Met His Thr Gly Asp Pro Lys Gln
92      20      25      30
93 Asp Leu Ala Tyr Glu Arg Gln Tyr Glu Gln Gln Thr Tyr Gln Val Ile
94      35      40      45
95 Pro Glu Val Ile Lys Asn Phe Ile Gln Tyr Phe His Lys Thr Val Ser
96      50      55      60
97 Asp Leu Ile Asp Gln Lys Val Tyr Glu Leu Gln Ala Ser Arg Val Ser
98 65      70      75      80
99 Ser Asp Val Ile Asp Gln Lys Val Tyr Glu Ile Gln Asp Ile Tyr Glu
100      85      90      95
101 Asn Ser Trp Thr Lys Leu Thr Glu Arg Phe Phe Lys Asn Thr Pro Trp
102      100      105      110
103 Pro Glu Ala Glu Ala Ile Ala Pro Gln Val Gly Asn Asp Ala Val Phe
104      115      120      125
105 Leu Ile Leu Tyr Lys Glu Leu Tyr Tyr Arg His Ile Tyr Ala Lys Val
106      130      135      140
107 Ser Gly Gly Pro Ser Leu Glu Gln Arg Phe Glu Ser Tyr Tyr Asn Tyr
108 145      150      155      160
109 Cys Asn Leu Phe Asn Tyr Ile Leu Asn Ala Asp Gly Pro Ala Pro Leu
110      165      170      175
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112				180					185					190		
113	Gln	Phe	Gln	Ser	Phe	Ser	Gln	Tyr	Arg	Cys	Lys	Thr	Ala	Lys	Lys	Ser
114			195					200					205			
115	Glu	Glu	Glu	Ile	Asp	Phe	Leu	Arg	Ser	Asn	Pro	Lys	Ile	Trp	Asn	Val
116		210					215					220				
117	His	Ser	Val	Leu	Asn	Val	Leu	His	Ser	Leu	Val	Asp	Lys	Ser	Asn	Ile
118	225				230						235					240
119	Asn	Arg	Gln	Leu	Glu	Val	Tyr	Thr	Ser	Gly	Gly	Asp	Pro	Glu	Ser	Val
120				245						250					255	
121	Ala	Gly	Glu	Tyr	Gly	Arg	His	Ser	Leu	Tyr	Lys	Met	Leu	Gly	Tyr	Phe
122			260					265						270		
123	Ser	Leu	Val	Gly	Leu	Leu	Arg	Leu	His	Ser	Leu	Leu	Gly	Asp	Tyr	Tyr
124			275					280					285			
125	Gln	Ala	Ile	Lys	Val	Leu	Glu	Asn	Ile	Glu	Leu	Asn	Lys	Lys	Ser	Met
126		290					295					300				
127	Tyr	Ser	Arg	Val	Pro	Glu	Cys	Gln	Val	Thr	Thr	Tyr	Tyr	Tyr	Val	Gly
128	305					310					315					320
129	Phe	Ala	Tyr	Leu	Met	Met	Arg	Arg	Tyr	Gln	Asp	Ala	Ile	Arg	Val	Phe
130				325						330					335	
131	Ala	Asn	Ile	Leu	Leu	Tyr	Ile	Gln	Arg	Thr	Lys	Ser	Met	Phe	Gln	Arg
132				340					345					350		
133	Thr	Thr	Tyr	Lys	Tyr	Glu	Met	Ile	Asn	Lys	Gln	Asn	Glu	Gln	Met	His
134			355				360						365			
135	Ala	Leu	Leu	Ala	Ile	Ala	Leu	Thr	Met	Tyr	Pro	Met	Arg	Ile	Asp	Glu
136		370					375					380				
137	Ser	Ile	His	Leu	Gln	Leu	Arg	Glu	Lys	Tyr	Gly	Asp	Lys	Met	Leu	Arg
138	385				390						395					400
139	Met	Gln	Lys	Gly	Asp	Pro	Gln	Val	Tyr	Glu	Glu	Leu	Phe	Ser	Tyr	Ser
140				405						410					415	
141	Cys	Pro	Lys	Phe	Leu	Ser	Pro	Val	Val	Pro	Asn	Tyr	Asp	Asn	Val	His
142				420					425					430		
143	Pro	Asn	Tyr	His	Lys	Glu	Pro	Phe	Leu	Gln	Gln	Leu	Lys	Val	Phe	Ser
144			435					440					445			
145	Asp	Glu	Val	Gln	Gln	Gln	Ala	Gln	Leu	Ser	Thr	Ile	Arg	Ser	Phe	Leu
146		450					455					460				
147	Lys	Leu	Tyr	Thr	Thr	Met	Pro	Val	Ala	Lys	Leu	Ala	Gly	Phe	Leu	Asp
148	465					470					475					480
149	Leu	Thr	Glu	Gln	Glu	Phe	Arg	Ile	Gln	Leu	Leu	Val	Phe	Lys	His	Lys
150				485						490					495	
151	Met	Lys	Asn	Leu	Val	Trp	Thr	Ser	Gly	Ile	Ser	Ala	Leu	Asp	Gly	Glu
152				500					505					510		
153	Phe	Gln	Ser	Ala	Ser	Glu	Val	Asp	Phe	Tyr	Ile	Asp	Lys	Asp	Met	Ile
154			515					520					525			
155	His	Ile	Ala	Asp	Thr	Lys	Val	Ala	Arg	Arg	Tyr	Gly	Asp	Phe	Phe	Ile
156		530					535					540				
157	Arg	Gln	Ile	His	Lys	Phe	Glu	Glu	Leu	Asn	Arg	Thr	Leu	Lys	Lys	Met
158	545					550					555					560
159	Gly	Gln	Arg	Pro												

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162 <210> SEQ ID NO: 3
163 <211> LENGTH: 1280
164 <212> TYPE: DNA
165 <213> ORGANISM: HOMO SAPIENS
167 <220> FEATURE:
168 <221> NAME/KEY: misc_feature
169 <223> OTHER INFORMATION: Incyte Clone No: 1240869
172 <400> SEQUENCE: 3

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175	acaaataagg	tggccctggt	aacggcctcc	accgacggga	tcggcttcgc	catcgcccgg	180
176	cgtttggccc	aggacagggc	ccacgtggtc	gtcagcagcc	ggaagcagca	gaatgtggac	240
177	caggcgggtg	ccacgctgca	gggggagggg	ctgagcgtga	cgggcaccgt	gtgccatgtg	300
178	gggaaggcgg	aggaccggga	gcggctggtg	gccacggctg	tgaagcttca	tggaggtatc	360
179	gatatacctag	tctccaatgc	tgctgtcaac	cctttctttg	gaagcataat	ggatgtcact	420
180	gaggaggtgt	gggacaagac	tctggacatt	aatgtgaagg	ccccagccct	gatgacaaag	480
181	gcagtgggtgc	cagaaatgga	gaaacgagga	ggcggctcag	tggtgatcgt	gtcttccata	540
182	gcagccttca	gtccatctcc	tggtctcagt	ccttacaatg	tcagtataaac	agccttgcctg	600
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184	gcacctggac	ttatcaagac	tagcttcagc	aggatgctct	ggatggacaa	ggaaaaagag	720
185	gaaagcatga	aagaaaccct	gcggataaga	aggttaggcg	agccagagga	ttgtgctggc	780
186	atcgtgtctt	tcctgtgctc	tgaagatgcc	agctacatca	ctggggaaac	agtgggtggtg	840
187	ggtggaggaa	ccccgtccc	cctctgagga	ccgggagaca	gccccacaggc	cagagttggg	900
188	ctctagctcc	tggtgctggt	cctgcattca	cccactggcc	tttcccacct	ctgctcacct	960
189	tactgttcac	ctcatcaaat	cagttctgcc	ctgtgaaaag	atccagcctt	ccctgccgtc	1020
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191	gagaacacag	gacaggcctg	ctgacaaggc	tgagtctacc	ttggcaaaga	ccaagatatt	1140
192	ttttcctggg	ccactgggga	atctgagggg	tgatgggaga	gaaggaaacct	ggagtgggaag	1200
193	gagcagagtt	gcaaattaac	aacttgcaaa	tgaggtgcaa	ataaaatgca	gatgattgcg	1260
194	cggttttgaa	aaaaaaaaaa					1280

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197 <211> LENGTH: 1894
198 <212> TYPE: DNA
199 <213> ORGANISM: HOMO SAPIENS
201 <220> FEATURE:
202 <221> NAME/KEY: misc_feature
203 <223> OTHER INFORMATION: Incyte Clone No: 2060002
205 <400> SEQUENCE: 4

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208	gcttatgaac	gtcagtatga	acagcaaacc	tatcagggtga	tccctgaggt	gatcaaaaac	180
209	ttcatccagt	atttccacaa	aactgtctca	gatttgattg	accagaaagt	gtatgagcta	240
210	caggccagtc	gtgtctccag	tgatgtcatt	gaccagaagg	tgtatgagat	ccaggacatc	300
211	tatgagaaca	gctggacca	gctgactgaa	agattcttca	agaatacacc	ttggcccagag	360
212	gctgaagcca	ttgctccaca	ggttggcaat	gatgctgtct	tcctgatttt	atacaaagaa	420
213	ttatactaca	ggcacatata	tgccaaagtc	agtgggggac	cttccttgga	gcagagggtt	480
214	gaatcctatt	acaactactg	caatctcttc	aactacattc	ttaatgccga	tggctctgct	540
215	ccccttgaac	tacccaacca	gtggctctgg	gatattatcg	atgagttcat	ctaccagttt	600
216	cagtcattca	gtcagtaccg	ctgtaagact	gccaaagaag	cagaggagga	gattgacttt	660

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217 cttcgttcca atcccaaaat ctggaatgtt catagtgtcc tcaatgtcct tcattccctg 720
218 gtagacaaat ccaacatcaa ccgacagttg gaggtatata caagcggagg tgaccctgag 780
219 agtgtggctg gggagtatgg gcggcactcc ctctacaaaa tgcttggtta cttcagcctg 840
220 gtcgggcttc tccgcctgca ctccctgtta ggagattact accaggccat caaggtgctg 900
221 gagaacatcg aactgaacaa gaagagtatg tattcccgtg tgccagagtg ccaggtcacc 960
222 acatactatt atgttgggtt tgcataattg atgatgcgtc gttaccagga tgccatccgg 1020
223 gtcttcgcca acatcctcct ctacatccag aggaccaaga gcatgttcca gaggaccacg 1080
224 tacaagtatg agatgattaa caagcagaat gagcagatgc atgcgctgct ggccattgcc 1140
225 ctcacgatgt accccatgcg tatcgatgag agcattcacc tccagctgcg ggagaaatat 1200
226 ggggacaaga tgttgccgat gcagaaagg gacccacaag tctatgaaga acttttcagt 1260
227 tactcctgcc ccaagttcct gtcgcctgta gtgcccaact atgataatgt gcacccaac 1320
228 taccacaaag agcccttcct gcagcagctg aaggtgtttt ctgatgaagt acagcagcag 1380
229 gccagctttt caaccatccg cagcttcctg aagctctaca ccaccatgcc tgtggccaag 1440
230 ctggctggct tcctggacct cacagagcag gagttccgga tccagcttct tgtcttcaaa 1500
231 cacaagatga agaacctcgt gtggaccagc ggtatctcag ccctggatgg tgaatttcag 1560
232 tcagcctcag aggttgactt ctacattgat aaggacatga tccacatcgc ggacaccaag 1620
233 gtcgccaggc gttatgggga tttcttcac cgtcagatcc acaaatttga ggagcttaat 1680
234 cgaaccctga agaagatggg acagagacct tgatgatatt cacacacatt caggaacctg 1740
235 ttttgatgta ttataggcag gaagtgtttt tgctaccgtg aaacctttac ctatgcagc 1800
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237 aaaggatctt tggagccaga aaaaaaaaaa aaaa 1894
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240 <211> LENGTH: 280

241 <212> TYPE: PRT

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244 <220> FEATURE:

245 <221> NAME/KEY: misc_feature

246 <223> OTHER INFORMATION: GENBANK ID: g1079566

248 <400> SEQUENCE: 5

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253 Val Leu Ala Asn Arg Val Ala Val Val Thr Gly Ser Thr Ser Gly Ile
254 35 40 45
255 Gly Phe Ala Ile Ala Arg Arg Leu Ala Arg Asp Gly Ala His Val Val
256 50 55 60
257 Ile Ser Ser Arg Lys Gln Gln Asn Val Asp Arg Ala Met Ala Lys Leu
258 65 70 75 80
259 Gln Gly Glu Gly Leu Ser Val Ala Gly Ile Val Cys His Val Gly Lys
260 85 90 95
261 Ala Glu Asp Arg Glu Gln Leu Val Ala Lys Ala Leu Glu His Cys Gly
262 100 105 110
263 Gly Val Asp Phe Leu Val Cys Ser Ala Gly Val Asn Pro Leu Val Gly
264 115 120 125
265 Ser Thr Leu Gly Thr Ser Glu Gln Ile Trp Asp Lys Ile Leu Ser Val
266 130 135 140
267 Asn Val Lys Ser Pro Ala Leu Leu Leu Ser Gln Leu Leu Pro Tyr Met
268 145 150 155 160
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VERIFICATION SUMMARY

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